

CLASS A GROUP II						
A1AB_human	α_{1B} -adrenergic alpha 1B-AR		TMDI	63 FAIVGNILVIL A	IP / COS-7	(Scheer, Faneli et al. 1997)
A1AB_human	α_{1B} -adrenergic alpha 1B-AR		junction between TMDIII and IC2	142 CAISIDRYIGV A		
A1AB_human	α_{1B} -adrenergic alpha 1B-AR		junction between TMDIII and IC2	143 CAISIDRYIGV K	IP / COS-7	(Scheer, Costa et al. 2000)
A1AB_human	α_{1B} -adrenergic		TMIII	128 AVDVLCTASI F	IP / COS-1	(Perez, Hwa et al. 1996)
			carboxyl end of IC3	293 REKKA A KTLLGI E	IP arachidonic acid release	
			TMV	204 EPPFYALFSSLG V	IP / COS-1	(Hwa, Gaivin et al. 1997)
A1AB_human	α_{1B} -adrenergic		C-terminal IC3	293 SREKKA A KT X=19 different substitutions	PI / COS-7	(Kjelsberg, Cotecchia et al. 1992)
A1AB_human	α_{1B} -adrenergic		C-terminus IC3	288 293 KFSREKKA A KTLLGI K H L	PI hydrolysis / rat fibroblast	(Allen, Lefkowitz et al. 1991)
A2AA_human	α_2C10 -adrenergic alpha-2AAR		C-terminal IC3 loop	373 (348?) EKRF T FVLAV X=F, A, C, E, K	adenyl cyclase inhibition / HEK293	(Ren, Kurose et al. 1993)
ACM1_human	muscarinic Hm1		C-terminal IC3 loop junction	360 SLVKEKKA A RTLLS A	PI / HEK(U293)	(Högger, Shockley et al. 1995)
ACM2_human	muscarinic acetylcholine M1 muscarinic acetylcholine M2		junction of IC3 and TMVI	390 KKVTRTIL 1 A 1-4 A inserted	IP production, inhibition of cAMP production / COS-7	(Liu, Blin et al. 1996)

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CLASS A GROUP II ACM3_rat	m3 muscarinic (rat)	TMVI	507 TWTPYNIMVLVNT S	IP / COS-7	(Blüml, Mutschler et al. 1994)
ACM5_human	muscarinic acetylcholine M3 m5 muscarinic	N-terminus to TMII TMVI	chimera composed of m2 1-69 m5 77-445 m2 391-466	β -gal / NIH 3T3	(Burststein, Spalding et al. 1996)
ACM5_human	muscarinic acetylcholine M5 m5 muscarinic	TMVI	451 459 465 AALLA EIIITW TPVNI MVLVST M L H C V S F T	β -gal; radioligand binding / NIH-3T3	(Spalding, Burststein et al. 1998)
ACM5_human	muscarinic acetylcholine M5 m5 muscarinic	junction of TMVI and EC3	465 YNIMVLVSTFCDKCV X=V,F,R,K,+more	β -gal; radioligand binding / NIH-3T3	(Spalding, Burststein et al. 1997)
B1AR_human	β_1 -adrenergic	C-terminus	389 RKAFOGLCCA R	adenylyl cyclase; agonist binding / CHW	(Mason, Moore et al. 1999)
B2AR_human	β_2 -adrenergic beta-2AR	C-terminal IC3 loop	266 272 FCLKEHKALKTGLI SR K A	adenylyl cyclase activation; agonist binding affinity / COS-7 or CHO	(Samama, Cotecchia et al. 1993); (Lefkowitz, Cotecchia et al. 1993)
DADR_human	dopamine D1A	carboxyl terminal IC3	264 SFKMSFKRET K VLKT I K 288 from D1B receptor APDTSIKKET K VLKT	adenylyl cyclase; cAMP accumulation / HEK293	(Charpentier, Jarvie et al. 1996)
DADR_human	dopamine D1	TMVI	286 FVCCWLPFFIL A	CAMP accumulation / COS-7	(Cho, Taylor et al. 1996)
HH2R_rat	histamine H ₂	IC2	115 FMISLDRYCAV N, A	cAMP production / HEK-293	(Alewijne, Timmerman et al. 2000)

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File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP III					
OPSD_human	opsin rhodopsin	TMII	90 FMVLGGFTSTLY D 113 GCNLEGGFFAT Q 292 296 MTIPAFFAKSAAIY E G, E, M 292 Ala neutral a.a converted to carboxylate and competes with ¹³ Glu for salt bridge with ²⁹⁶ Lys	transducin; phosphorylation by rhodopsin kinase / COS	(Rim and Oprian 1995)
		TMIII			
		TMVII			
OPSD_human	opsin rhodopsin	TMIII	134 VVLAIERYVVV I, Q, S	transducin; radioligand binding / COS	(Acharya and Karnik 1996)
OPSD_human	opsin rhodopsin	TM6	257 RMVIIMVIAFL Y, N	transducin, GTPγS uptake / COS	(Han, Smith et al. 1998)
OPSD_human	opsin rhodopsin	plus TM3 TMVII	plus G113Q 296 PAFFAKSAAIY G X=E,M natural mutants + 10 different a.a. substitutions disrupts critical salt bridge between ²⁹⁶ Lys(TMVII) and ¹¹³ Glu(TMIII)	transducin; radioligand binding / COS	(Govardhan and Oprian 1994); (Cohen, Yang et al. 1993)
		IC2	134 VVLAIERYVVV Q		(Cohen, Yang et al. 1993)

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TRFR_mouse	thyrotropin-releasing hormone TRH-R	carboxyl tail	335 FRKL C NCCKQK STOP	⁴⁵ Ca ²⁺ efflux, [Ca ²⁺] / Xenopus oocytes; IP formation / AtT20, <i>stably transfected</i>	(Matus-Leibovitch, Nussenzveig et al. 1995)

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP IV BRB2_human	bradykinin B ₂ B2 bradykinin BK-2	TMIII TMVI	<div> <div>113</div> <div>ATISMNLYSSI</div> <div>A</div> <div>256</div> <div>LLFIICWLPFQI</div> <div>F</div> </div>	IP production / COS-7	(Marie, Koch et al. 1999)

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP V					
AG2R_rat	AT _{1A} Type-1A angiotensin II	TMIII	111 ASVSFNL _A YASV disrupts ¹¹¹ Asn(TMIII) - ²⁹² Tyr(TMVII) interaction	phospholipase C; IP production / COS-7	(Grobowski, Maigret et al. 1997)
AG2R_rat	AT _{1A}	C-terminus of TM7	305 LFYGF _Q L _Q GKKFK	IP production / HEK-293; intracellular Ca ²⁺ mobilization / CHO	(Parnot, Bardin et al. 2000)
FMLR_human	Type-1A angiotensin II formylmethionylleucylphenylalanine (fMLPR)	other multiple mutations IC1	51 LV _W VAGFRMTH _Y TVTTIS _Y LNKAVA LV _W VTAF _E AKRTINAIWFLNLAVA (K above conflicts with SWISS-PROT database)	PI production; phospholipase C stimulation / COS-7	(Amatuda, Dragas-Graonic et al. 1995)
IL8B_human	interleukin-8 receptor B	IC2	138 ACISV _D RYLAIV _H	IP production; Ca ²⁺ mobilization and actin polymerization / NIH 3T3	(Burger, Burger et al. 1999)
LSHR_human	CXCR-2 chemokine	IC3	564 MATNK _D TKIAK _K	cAMP production / HEK293	(Kudo, Osuga et al. 1996)
LSHR_human	luteinizing hormone (LH)	TMVI	578 ILIFT _D FT _G CM _A	cAMP production / COS-7	(Shenker, Laue et al. 1993)
LSHR_human	luteinizing hormone (LH)	TM6	571 577 KIAK _K MAILIFT _D FT _I CM _I	cAMP production / COS-7	(Kosugi, Van Dop et al. 1995)
LSHR_rat	luteinizing hormone / human chorionic gonadotropin (LH/hCG)	TMVI	556 ILIFT _D FT _G CM _A G, Y	cAMP production / HEK 293T	(Bradbury, Kawate et al. 1997; Bradbury and Menon 1999)
OPRD_mouse	delta opiod receptor	TM3	128 KVLSD _I Y _N NMF A, K, H	adenyl cyclase inhibition / COS-7	(Cavalli, Babey et al. 1999)
OXYR_human	oxytocin	IC2	137 LMSLD _R CLAIC _A	IP production / COS-7	(Fanelli, Barbier et al. 1999)

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PAFR_human	platelet-activating factor (PAF)	C-terminus of IC3	231 EVKRRALMMVCTVLAV R	IP production / COS-7	(Parent, Le Gouill et al. 1996)
PAFR_human	platelet-activating factor (PAF)	TMIII	100 CLFFINTYCSV A	arachidonate release, IP production, adenylyl cylcase inhibition / CHO	(Ishii, Izumi et al. 1997)
PE23_human	prostaglandin E ₃ , EP3III EP3IV	C-terminal tail	360 FCOEFFWGN FCOMRKRRRLREOEFFWGN ↑truncated	inhibition of adenylyl cyclase / CHO-K1	(Jin, Mao et al. 1997)
PE23_mouse	prostaglandin E ₃ , EP3	carboxyl-terminal tail	336 KILLRKFCQIRDHT (3α) MMNHL (3β) ↑truncated	inhibition of adenylyl cyclase / CHO, <i>stably expressed</i>	(Hasegawa, Negishi et al. 1996)
THRR_human	thrombin	EC2 loop	259 268 CHDVLN ETLL EGYYAY DLKD KDF I	⁴⁵ Ca ²⁺ efflux, PI hydrolysis, reporter gene induction / COS-7	(Nanevicz, Wang et al. 1996)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	EC1 EC2	486 YYNHAI DWQTG F, M 568 YAKVS I CLPMD T	inositol phosphate-- diacylglycerol cascade / COS-7	(Parma, Van Sande et al. 1995)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	TMIII TMVII	509 ASELS VYTLTV A 672 YPLNSCANPFL Y	adenylyl cyclase activation / COS-7	(Duprez, Parma et al. 1994)
TSHR_human	thyrotropin (TSHR)	TMV	597 VAFVI VCCCHV L	cAMP formation / COS-7 cells	(Esapa, Duprez et al. 1999)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	TMVII	677 CANPFL Y AIFT V	cAMP formation / CHO cells	(Russo, Wong et al. 1999)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	IC3	613 621 VRNPQYN PGDKDT KIAK deletion	cAMP formation / COS-7	(Wonerow, Schoneberg et al. 1998)

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TSHR_human	thyrotropin (TSHR)	IC3 / TMVI	623 KDTKIAKRMVAVLIFTDFICM V I	cAMP activation / COS-7	(Paschke, Tonacchera et al. 1994)
V2R_human	thyroid stimulating hormone vasopressin V2	IC2	136 LAWTLDRHRAI A	cAMP formation / COS-7	(Morin, Cotte et al. 1998)

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File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS B GROUP I					
CALR_human	human calcitonin hCTR-1	wild type (native) protein		adenyl cyclase cAMP production / COS-1	(Cohen, Thaw et al. 1997)
CLASS B GROUP II					
PTRR_human	parathyroid hormone PTH / PTH-related peptide	junction of IC1 and TMII	223 TRNYIH ^H HLFL R, K	cAMP accumulation / COS-7	(Schipani, Jensen et al. 1997)
		junction of IC3 and TMVI	410 KLLKST ^L VLMP C, others		
CLASS B GROUP III					
GIPR_human	glucose-dependent insulinotropic peptide (GIP-R)	TMVI	340 VFAPV ^T EEQAR P	cAMP production / L293	(Tseng and Lin 1997)
GLR_rat	glucagon	junction of IC loop I and TMII	178 TRNYIH ^H GNLFA R	cAMP accumulation / COS-7	(Hjorth, Orskov et al. 1998)
		IC end of TMVI	352 RLARST ^L LLIP A		
VIPR_human	vasoactive intestinal peptide 1 (VIP)	junction of IC loop 1 and TMII	178 RNYIH ^H HLFI R requires functional integrity of the N-terminal EC domain	cAMP production / COS-7 or CHO	(Gaudin, Maoret et al. 1998) (Gaudin, Rouyer-Fessard et al. 1998)
		junction of IC loop 3 and TMVI	343 LARST ^L LLIP X= K, P		

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File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS C					
CASR_human	calcium-sensing	N-terminal EC	TLSPVAQNKIDSLNLDFCNCSEHI various substitutions, in multiple combinations	IP / tsA	(Jensen, Spalding et al. 2000)

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File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS D					
O74283	pheromone	TM6	229 PLSAYQIYLGT P	heterologous yeast assay	(Olesnicky, Brown et al. 1999)
RCB2					
C. cinereus					
STE2_yeast	pheromone α -factor	TM6	258 QSLLVPSIIFI LL	<i>lacZ</i> reporter gene	(Konopka, Margarit et al. 1996)
STE2_yeast	pheromone α -factor	double mutations TM5 and TM6	223 MSFVLVVKVILAIR C C 247 251 DSFHILLMSQSL CC CC double mutations TM5 and TM6	<i>lacZ</i> reporter gene / yeast	(Dube, DeCostanzo et al. 2000)
STE3_yeast	pheromone α -factor	IC3	194 DVRDILHCTNS Q	β -galactosidase	(Boone, Davis et al. 1993)
STE2_yeast	pheromone α -factor	TM6	253 258 LIMSCQSLLVPSIIFI L LP	β -galactosidase	(Sommers, Martin et al. 2000)

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Light Emission Induced by the WT CCK-BR vs. a Constitutively Active Mutant

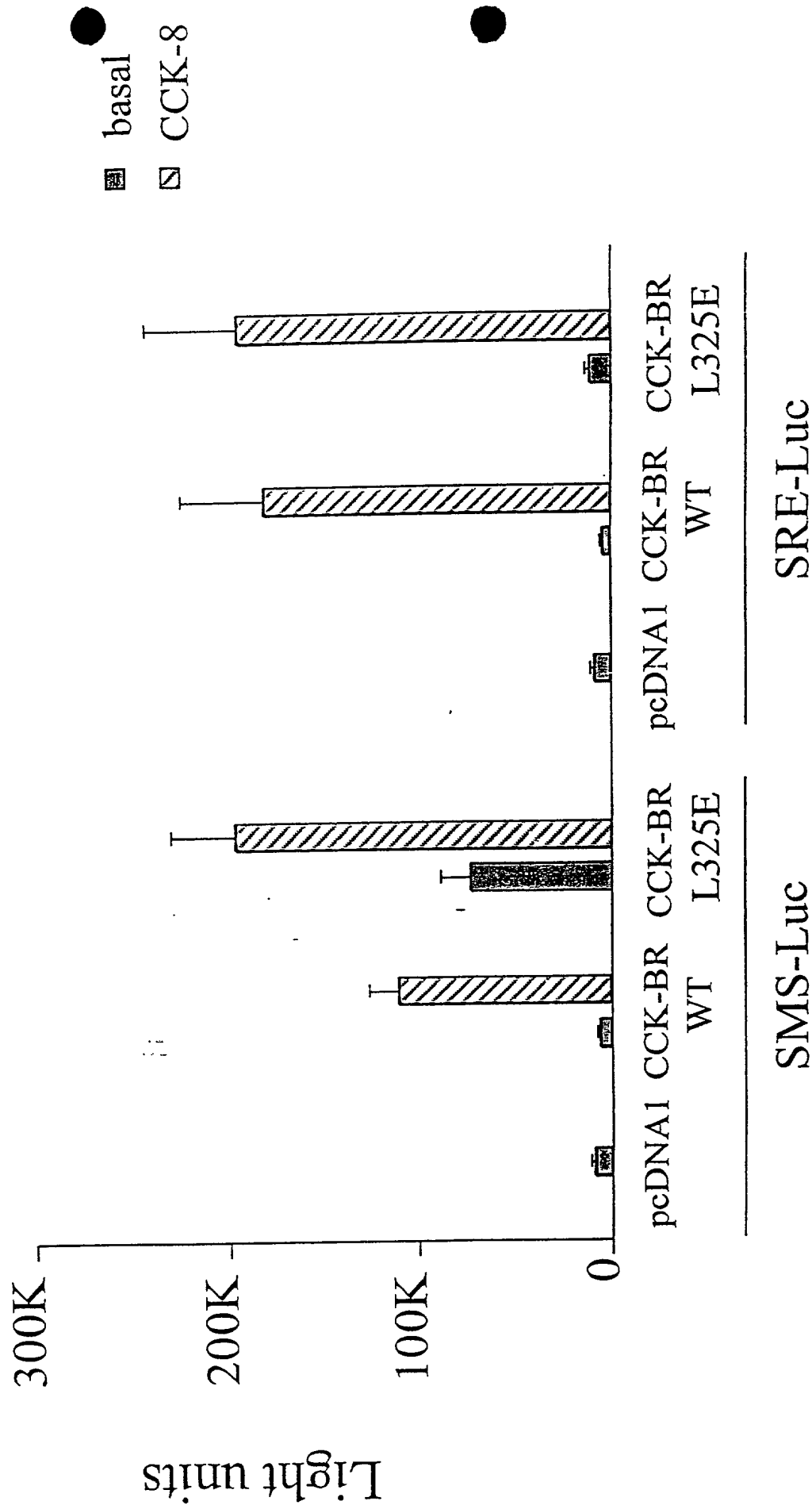


Figure 2

A Point Mutation Confers Constitutive Activity to the Rat μ Opioid Receptor

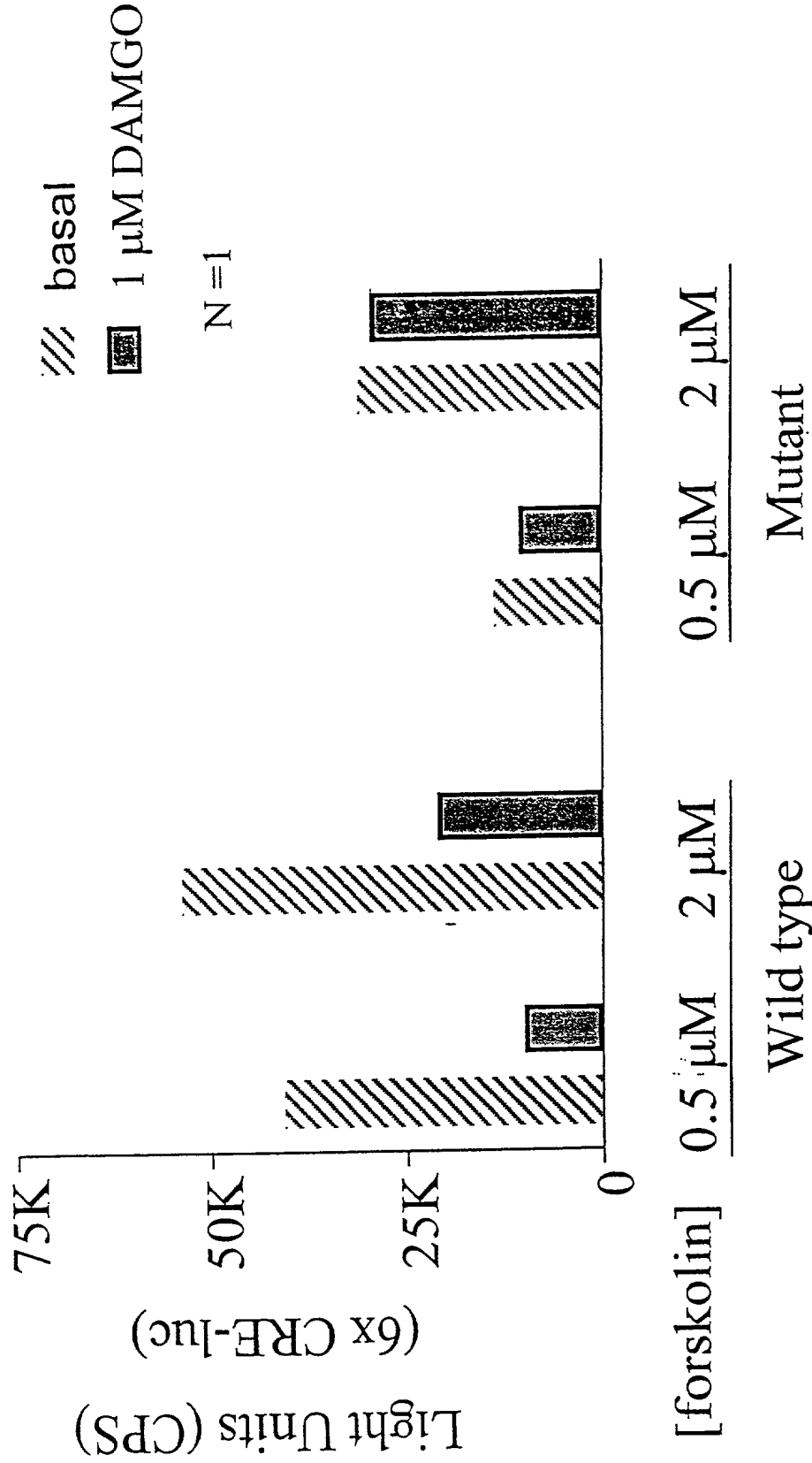


Figure 3

Forskolin Stimulated HEK293 Cells Transfected With pcDNA1 and a CRE-luc Construct

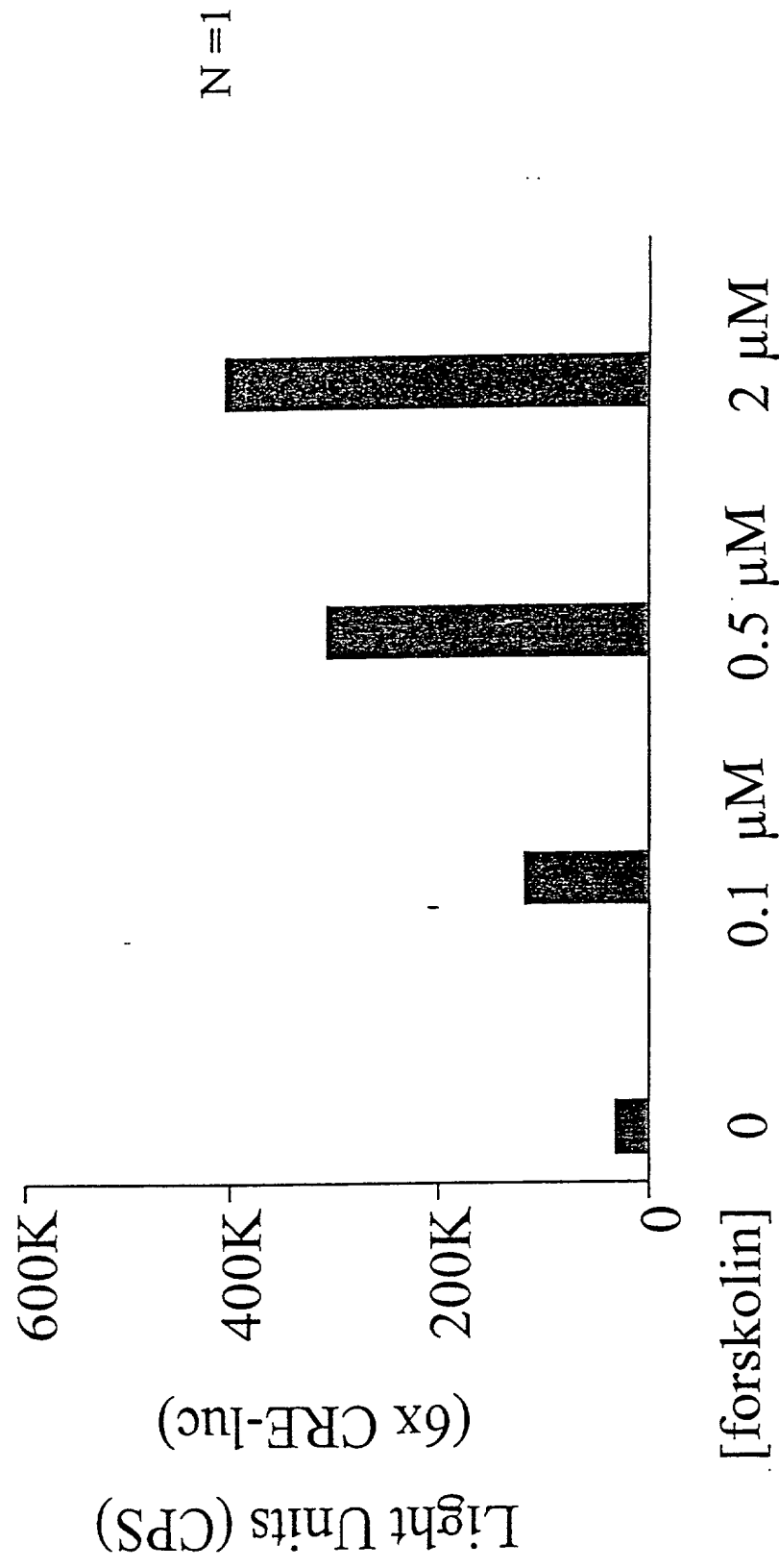


Figure 4

The Rat μ Opioid Receptor Signals Through G α i

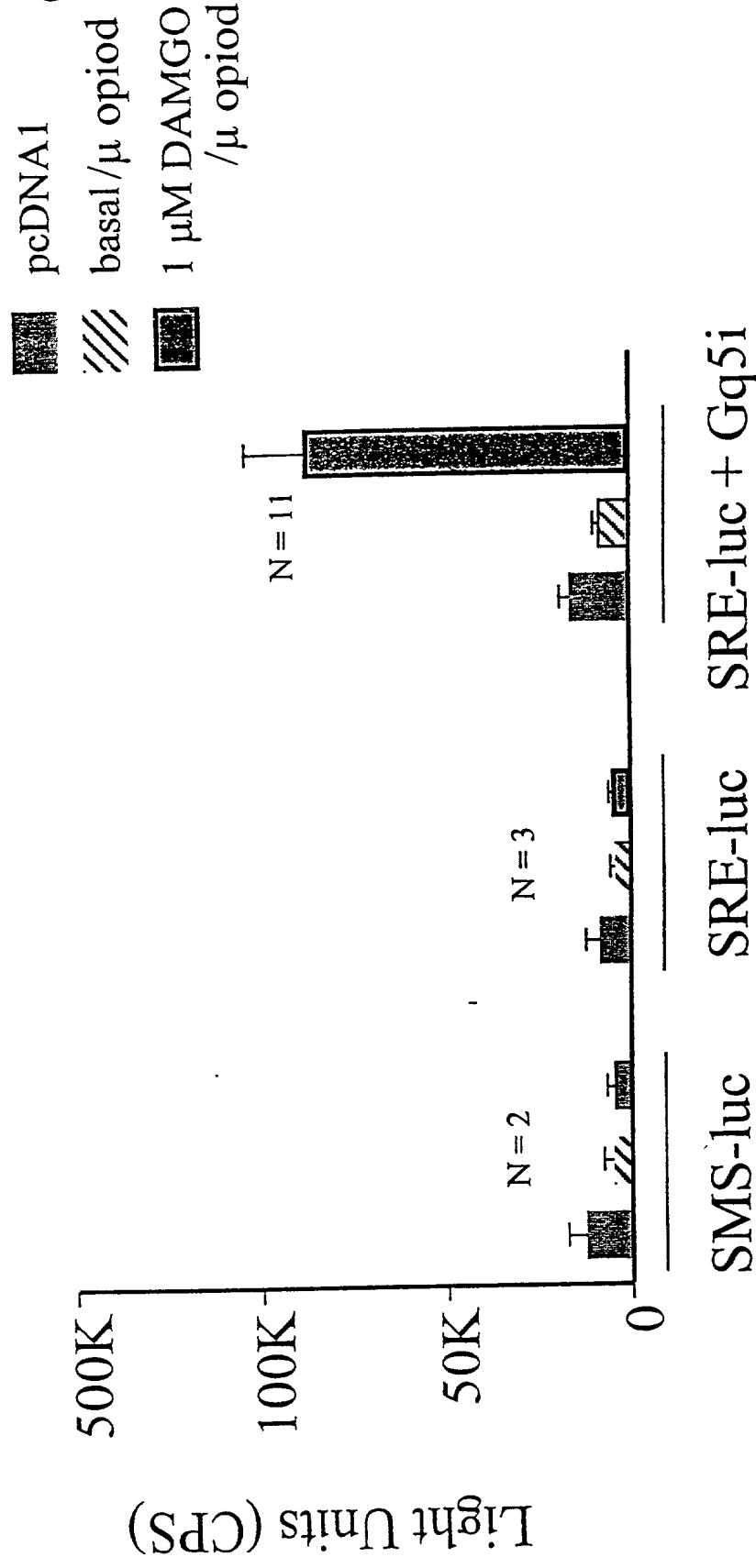


Figure 5

A Point Mutation Confers Constitutive Activity to the Rat μ Opioid Receptor

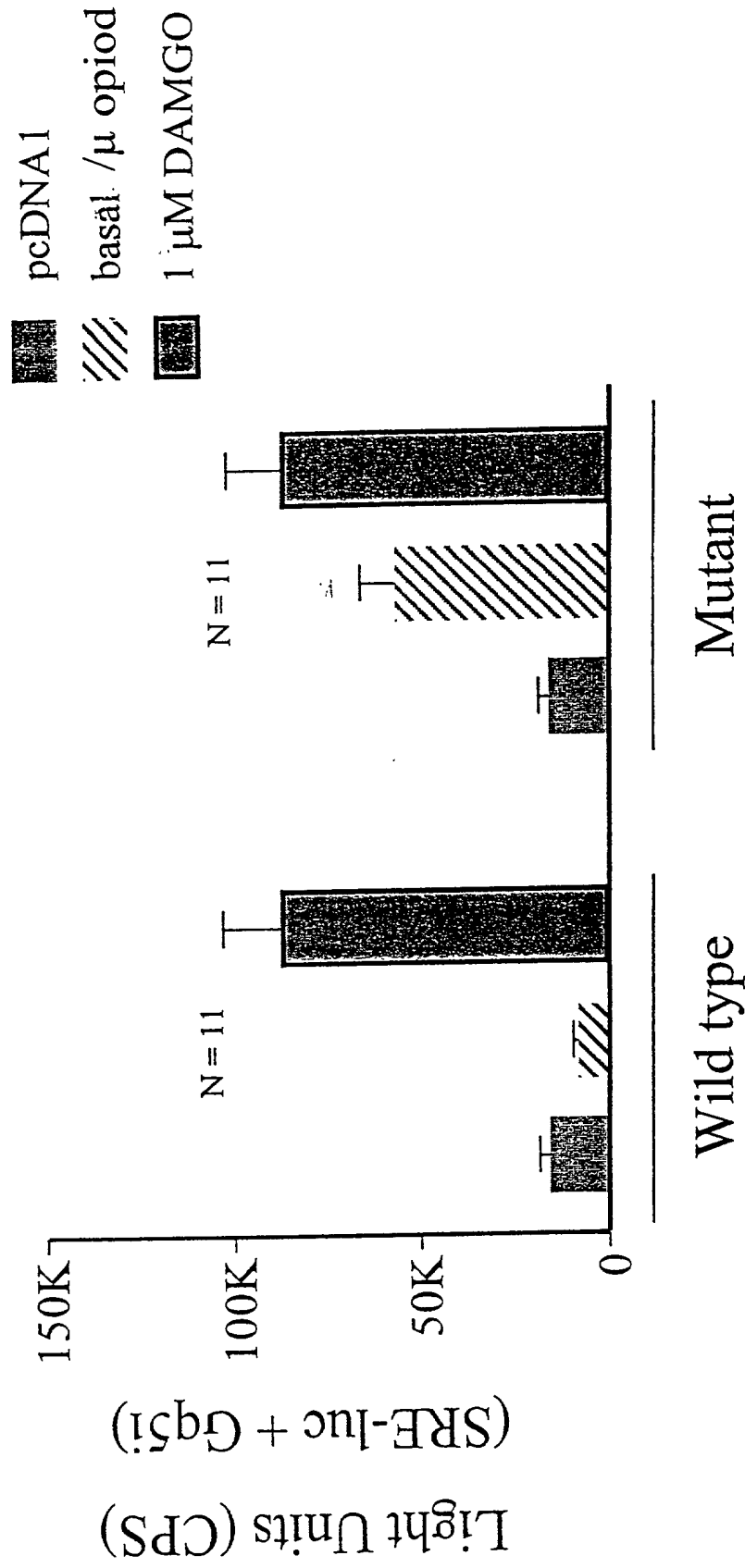


Figure 6

Target Residues Within Class I GPCRs

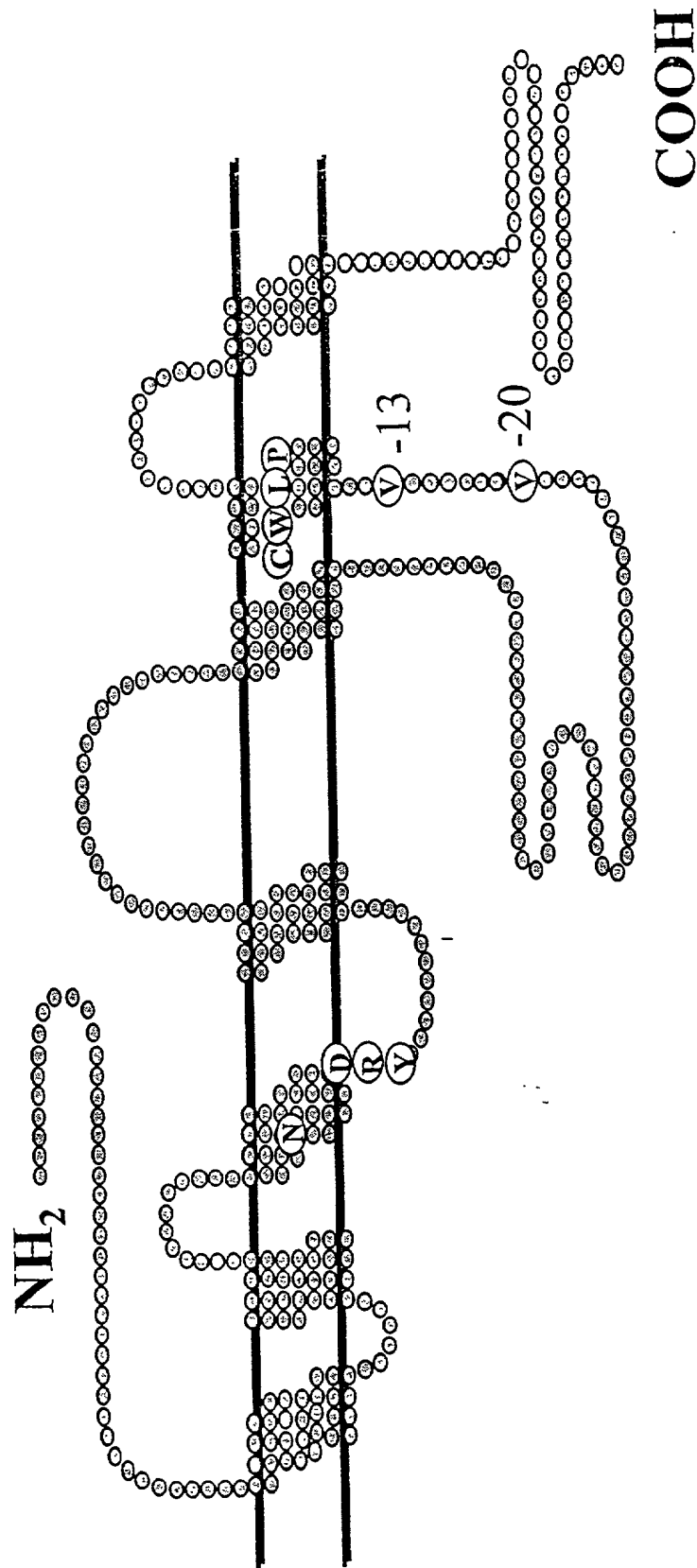
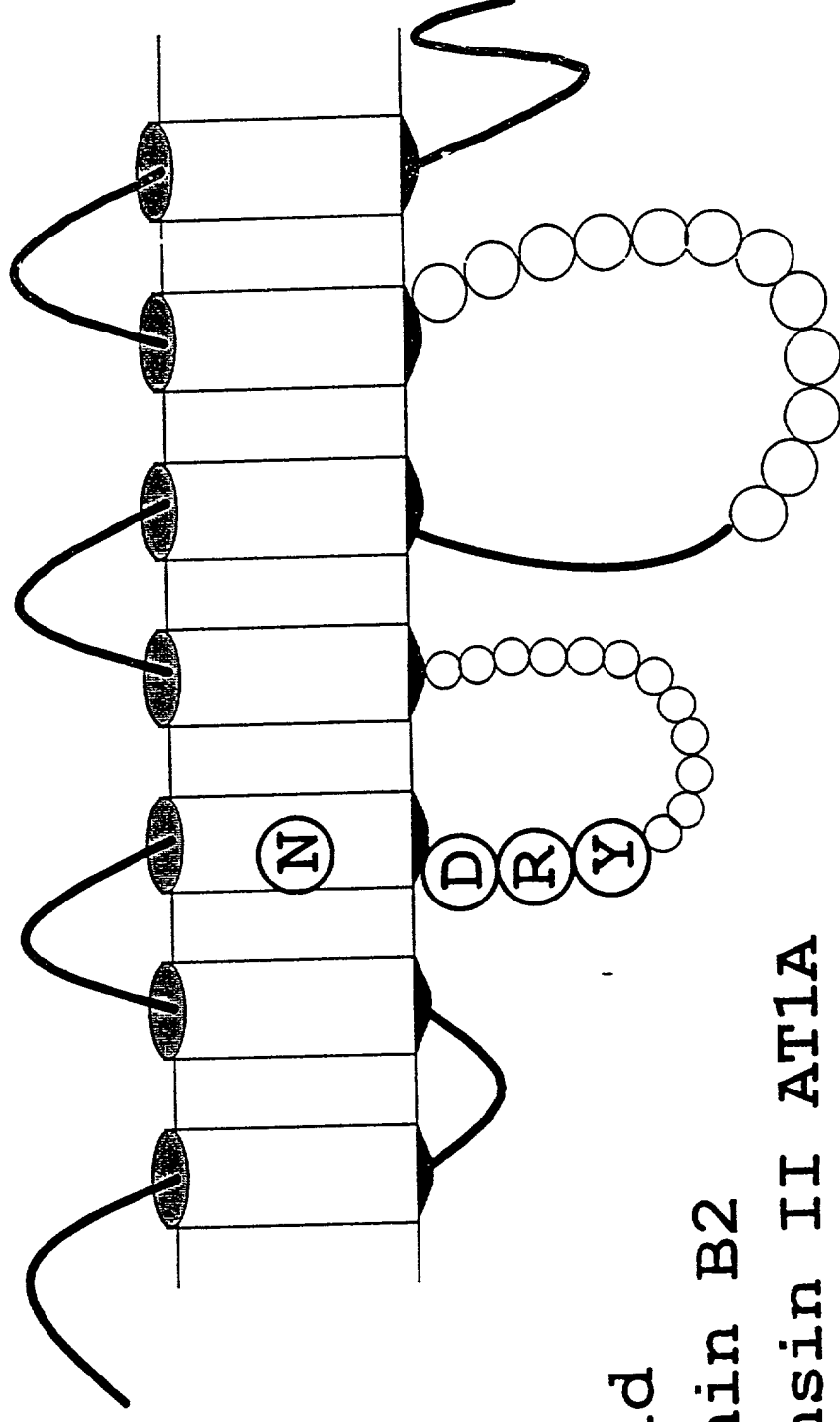


Figure 7

TMD III Asn (-14 from DRY) is a Target for Mutation Induced Constitutive Activity



mu opioid
bradykinin B2
angiotensin II AT1A

Figure 8

The 'DRY' Motif is a Target for Mutation Induced Constitutive Activity

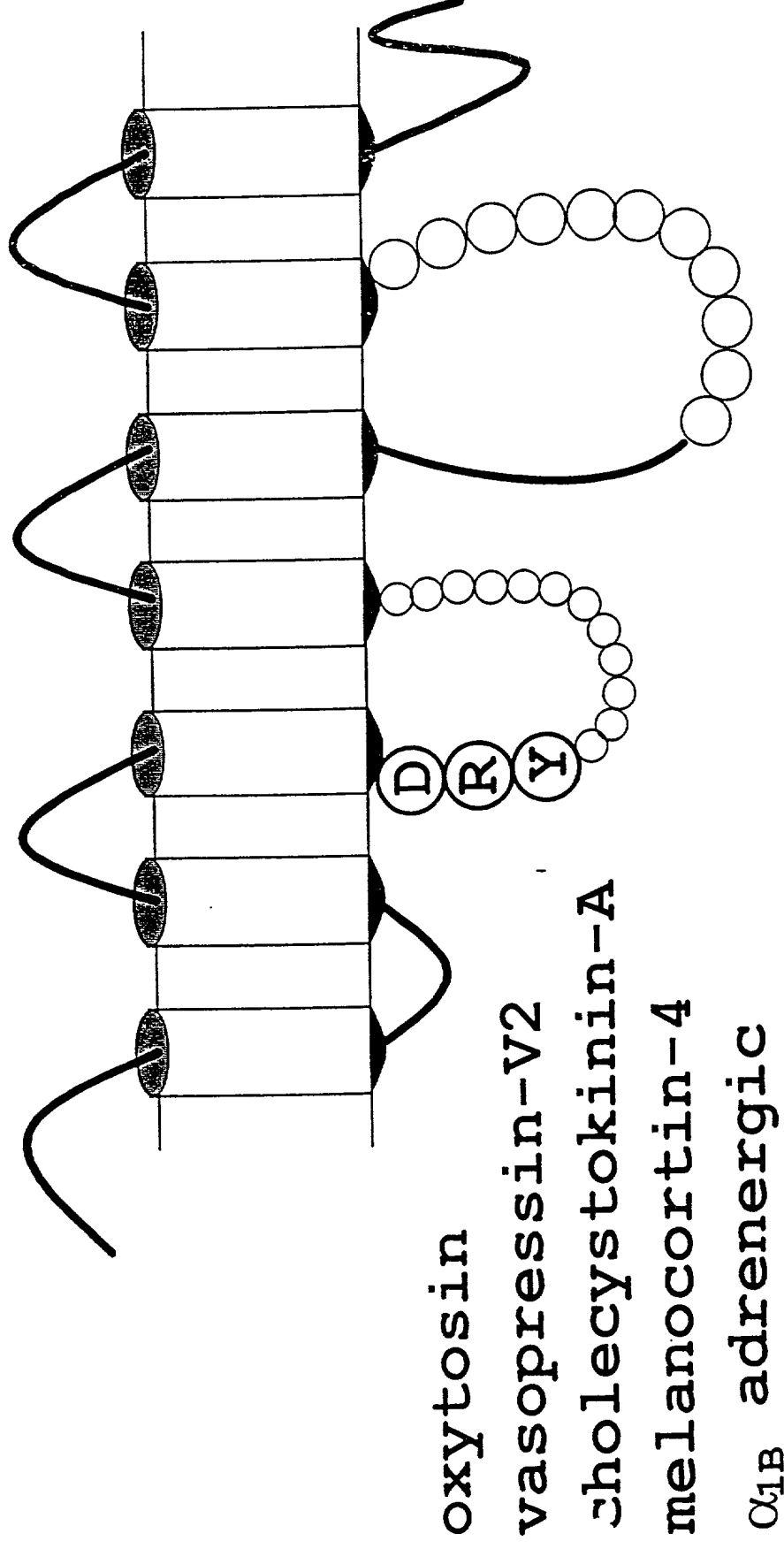


Figure 9

A Point Mutation Enhances MC-4 Receptor Constitutive Activity

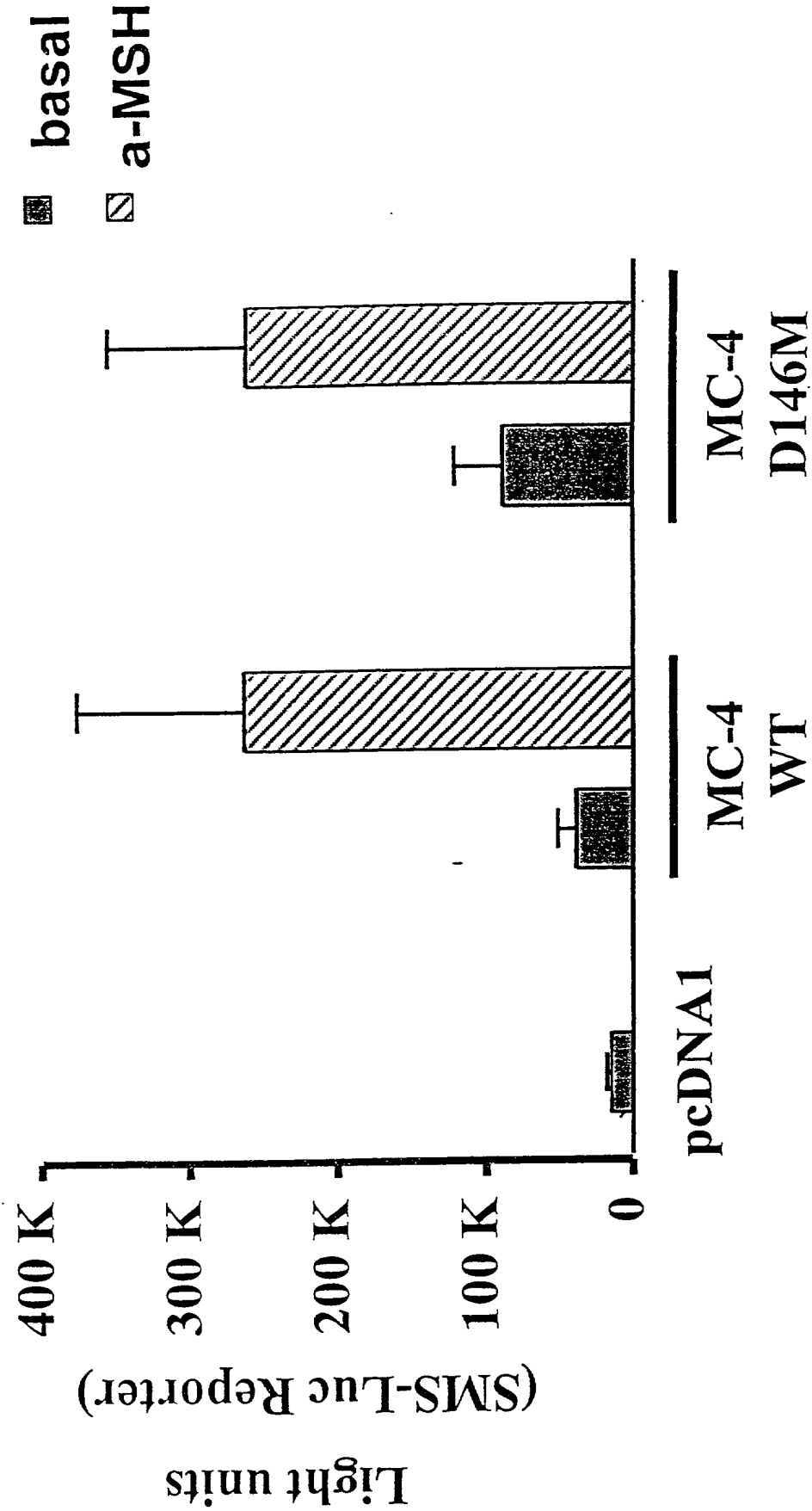
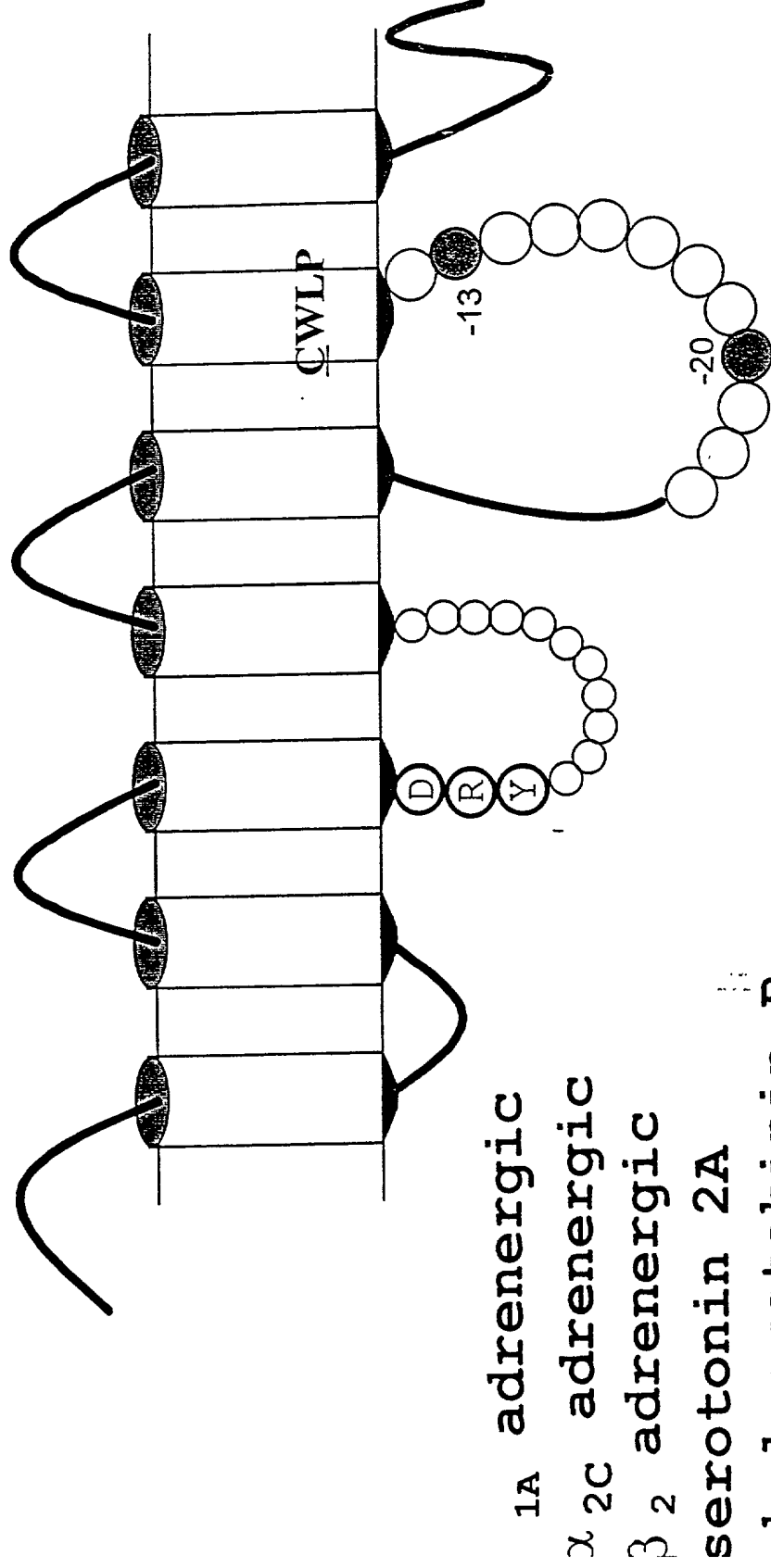


Figure 10

The -13 Position is a Target for Mutation Induced Constitutive Activity



1A adrenergic
 2C adrenergic
 3 2 adrenergic
 serotonin 2A
 cholecystokinin-B
 platelet activating factor
 thyroid stimulating hormone

Figure 11

0966671-0966671

```

ork 1 -----MESP-----FRGEPGETCAPSACTPPNSSAWFPGWASP-----SNGSAGSSEDAQ
orkr 1 -----MESPIQ-----FRGEPGETCAPSACTLPMSSSWFPPNWAES...DSNGSVGSEDDQ
orm 1 MDSSAAPTNASNCTDAAYSSCSBAPSPGSGW...NLSHLDENLSDPCGPNRTDLGGRDSL
ormr 1 MDSSTGPGNTSDCSDPFAQASCSEA...PGSWL...NLSHVDENQSDPCGLNRTGLGNDL
ord 1 -----MEBAPSAGAE...PPLFNNASDAYPSACPSACANASG
AT1a 1 -----MALNSSAEDCIKRIQ
BK-2 1 -----MFSPWKISMFLSVREDSVPTTASFSAADMLNVTLQGPTLNG.TFAQ

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ork 49 LEPAHISEAT...PUBITANYSVVEVVLGAGNSLVMEVIRYTKMKATATNYIFNLALADA
orkr 49 LEPAHISEAT...PUBITANYSVVEVVLGAGNSLVMEVIRYTKMKATATNYIFNLALADA
orm 59 CPPTGS...ESMITAHTIMALYSHVVCVGLFGNFLVMVIRYTKMKATATNYIFNLALADA
ormr 57 CPQTGS...ESMVTATHTIMALYSHVVCVGLFGNFLVMVIRYTKMKATATNYIFNLALADA
ord 37 PPGARSASSALAHATIALYSACVAGLFGNFLVMVIRYTKMKATATNYIFNLALADA
AT1a 16 DDCPRAGRHSYIFVPTDYSIEFVCHFGNSLVVIVYFYMKKIVASVIFNLALADL
BK-2 45 SKCPQVEWLGLWNTQPPFLWVFEVATBENIFVLSVFLHKSSCTVAEIVIFNLALADL

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ork 107 LVTHTTFFQSTVYLMN...SWPFGHILCKIVISIDYNNMFTSIFTLTMSVDRYIAVCHPVK
orkr 107 LVTHTTFFQSAVYLMN...SWPFGHILCKIVISIDYNNMFTSIFTLTMSVDRYIAVCHPVK
orm 118 LANSILPEFOSANVLMG...SWPFGHILCKIVISIDYNNMFTSIFTLCTMSVDRYIAVCHPVK
ormr 116 LANSILPEFOSANVLMG...SWPFGHILCKIVISIDYNNMFTSIFTLCTMSVDRYIAVCHPVK
ord 97 LANSILPEFOSAKYLMG...SWPFGHILCKIVISIDYNNMFTSIFTLTMSVDRYIAVCHPVK
AT1a 76 CFLLTLELWAVYTAMEYRDPFCHILCKIASASVTENTYASMLLTCCHSDRYIAVCHPVK
BK-2 105 ILACGLPEFWAITISNNFDWLRGFTLCRAVNAHISMNLYSSICFLMAYSDRYIAVCHPVK

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↑ from DRY *

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ork 166 ALDERTELKAKTINICHWLSSVCHSAIVLGGTKVR...EDVDVIECSLOFEDDDYSWWD
orkr 166 ALDERTELKAKTINICHWLSSVCHSAIVLGGTKVR...EDVDVIECSLOFEDDDYSWWD
orm 177 ALDERTERNAKTINICHWLSSVCHSAIVLGGTKVR...Q...GSIDCHLTHSPTW.YWE
ormr 175 ALDERTERNAKTINICHWLSSVCHSAIVLGGTKVR...Q...GSIDCHLTHSPTW.YWE
ord 156 ALDERTEPAKAKTINICHWLSSVCHSAIVLGGTKVR...D...GAVVCHLTHSPTW.YWD
AT1a 136 SRLRETLMLVAKYTCIIILWLAGLASDEAVHNRV...YFIENTNITVCAFHYESRN.STLP
BK-2 165 MGRMGVRWAKYSLVITWGCLLLSSPMVFRMTKEYSDEGHNVTAQVLSHPS...LIWE

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ork 224 LFWKICVEIFAEVPEVLIITVCYGLMLRLKSVRLSGSKEKDRNLRRITRNLVWVAVE
orkr 224 LFWKICVEIFAEVPEVLIITVCYGLMLRLKSVRLSGSKEKDRNLRRITRNLVWVAVE
orm 232 NLKICVEIFAEVPEVLIITVCYGLMLRLKSVRLSGSKEKDRNLRRITRNLVWVAVE
ormr 230 NLKICVEIFAEVPEVLIITVCYGLMLRLKSVRLSGSKEKDRNLRRITRNLVWVAVE
ord 211 TVTKICVEIFAEVPEVLIITVCYGLMLRLKSVRLSGSKEKDRNLRRITRNLVWVAVE
AT1a 193 IGLGETKNILGELFPFLITTSYTLWKALKAYEIQKNKPRND...IFRILMAIVLFF
BK-2 222 VFTNMLNIVVGHLEP.LSVITFCIMQIMOLRNEMOKFKEIQTE.RRATVILVWVLLLE

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ork 284 IVCWTPIHIFVWVWALGS.T....SHSIAALSSMYECIALGYTNSSLNPHLYAFLDENF
orkr 284 IVCWTPIHIFVWVWALGS.T....SHSIAALSSMYECIALGYTNSSLNPHLYAFLDENF
orm 292 IVCWTPIHIFVWVWALGS.T....SHSIAALSSMYECIALGYTNSSLNPHLYAFLDENF
ormr 290 IVCWTPIHIFVWVWALGS.T....SHSIAALSSMYECIALGYTNSSLNPHLYAFLDENF
ord 271 IVCWTPIHIFVWVWALGS.T....SHSIAALSSMYECIALGYTNSSLNPHLYAFLDENF
AT1a 250 FFSWVPHQIFTFLEVLLQGVHDCIKSDIOTAMPITICTAYFNNCLNPLFYGLGKKE
BK-2 280 IVCWLPFOISTFILTIRHILGILSSCODERIIDVITQIASFMAYNSCLNPLVWVWVGRF

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SEQ ID NO:

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ork 338 KRCFRDFCFPIKMRMBROSISRAR.NIVOD.PAYLRDIDGMNKPV----- 76
orkr 338 KRCFRDFCFPIKMRMBROSISRAR.NIVOD.PASMRDVGGMNKPV----- 77
orm 346 KRCFRDFCFIPTSSNHEOONSIRARONT.RDHPSIANTVDRTNHELENLEAETAPLP 78
ormr 344 KRCFRDFCFIPTSSNHEOONSIRARONT.RDHPSIANTVDRTNHELENLEAETAPLP 79
ord 326 KRCFRDFCFIPTSSNHEOONSIRARONT.RDHPSIANTVDRTNHELENLEAETAPLP 80
AT1a 310 KRYELQLLLKYIUPPKAKSHS...SLSTKM...STLSYRPSDNMSSSAKKPASCPEVE- 81
BK-2 340 RKKSWEVYQGVCKGGCRSEPIOMENSM..GTL..RTSISVERQIHKLDWAGSRQ 82

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Figure 12

09966671.092801

mORmouse 1 MDSSAGEGNTSDSDPIA.PLSQSPA...EGSWHMLSHMDGMSDPOGPNRTGLGGSLSLO
mORrat 1 MDSSAGEGNTSDSDPIA.QASQSPA...EGSWHMLSHMDGMSDPOGPNRTGLGGSLSLO
mORbovin 1 MDSSAGEGNTSDSDPIA.QASQSPA...EGSWHMLSHMDGMSDPOGPNRTGLGGSLSLO
mORhuman 1 MDSSAGEGNTSDSDPIA.QASQSPA...EGSWHMLSHMDGMSDPOGPNRTGLGGSLSLO
mORpig 1 MDSSAGEGNTSDSDPIA.QASQSPA...EGSWHMLSHMDGMSDPOGPNRTGLGGSLSLO
mORws 1 MDSSAGEGNTSDSDPIA.QASQSPA...EGSWHMLSHMDGMSDPOGPNRTGLGGSLSLO
ATla 1 MDSSAGEGNTSDSDPIA.QASQSPA...EGSWHMLSHMDGMSDPOGPNRTGLGGSLSLO
BK-2 1 MDSSAGEGNTSDSDPIA.QASQSPA...EGSWHMLSHMDGMSDPOGPNRTGLGGSLSLO

mORmouse 58 EOTGSPSMITAITINALYSIVCVGLFGNFWMYVIVRYTKMKTATNITYTENLALADALA
mORrat 58 EOTGSPSMITAITINALYSIVCVGLFGNFWMYVIVRYTKMKTATNITYTENLALADALA
mORbovin 61 EOTGSPSMITAITINALYSIVCVGLFGNFWMYVIVRYTKMKTATNITYTENLALADALA
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mORpig 61 EOTGSPSMITAITINALYSIVCVGLFGNFWMYVIVRYTKMKTATNITYTENLALADALA
mORws 48 EOTGSPSMITAITINALYSIVCVGLFGNFWMYVIVRYTKMKTATNITYTENLALADALA
ATla 19 EOTGSPSMITAITINALYSIVCVGLFGNFWMYVIVRYTKMKTATNITYTENLALADALA
BK-2 48 EOTGSPSMITAITINALYSIVCVGLFGNFWMYVIVRYTKMKTATNITYTENLALADALA

mORmouse 118 TSTLPFQSVNYLMG...TWPEGNLLCKIVISIDYNNMFTSIFTLCIMSVDRIYAVCHPVKAL
mORrat 118 TSTLPFQSVNYLMG...TWPEGNLLCKIVISIDYNNMFTSIFTLCIMSVDRIYAVCHPVKAL
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ATla 78 TSTLPFQSVNYLMG...TWPEGNLLCKIVISIDYNNMFTSIFTLCIMSVDRIYAVCHPVKAL
BK-2 107 TSTLPFQSVNYLMG...TWPEGNLLCKIVISIDYNNMFTSIFTLCIMSVDRIYAVCHPVKAL

mORmouse 177 DERTPRNAKIVAVCNWILSSAIGLPVMMFATTKYRQ.....GSIDCLTFSSHPTWYWE
mORrat 177 DERTPRNAKIVAVCNWILSSAIGLPVMMFATTKYRQ.....GSIDCLTFSSHPTWYWE
mORbovin 180 DERTPRNAKIVAVCNWILSSAIGLPVMMFATTKYRQ.....GSIDCLTFSSHPTWYWE
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ATla 138 DERTPRNAKIVAVCNWILSSAIGLPVMMFATTKYRQ.....GSIDCLTFSSHPTWYWE
BK-2 167 DERTPRNAKIVAVCNWILSSAIGLPVMMFATTKYRQ.....GSIDCLTFSSHPTWYWE

mORmouse 230 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVVAVF
mORrat 230 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVVAVF
mORbovin 233 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVVAVF
mORhuman 232 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVVAVF
mORpig 233 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVVAVF
mORws 226 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVVAVF
ATla 193 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVVAVF
BK-2 222 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVVVAVF

mORmouse 290 IVCWTPRIHYVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENE
mORrat 290 IVCWTPRIHYVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENE
mORbovin 293 IVCWTPRIHYVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENE
mORhuman 292 IVCWTPRIHYVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENE
mORpig 293 IVCWTPRIHYVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENE
mORws 286 IVCWTPRIHYVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENE
ATla 250 IVCWTPRIHYVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENE
BK-2 280 IVCWTPRIHYVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENE

mORmouse 344 KRCFREFO...IPTSSSTIEQONSARIRONTREHPSTANTVDRTNHOLENLEAETAPLE 83
mORrat 344 KRCFREFO...IPTSSSTIEQONSARIRONTREHPSTANTVDRTNHOLENLEAETAPLE 79
mORbovin 347 KRCFREFO...IPTSSSTIEQONSARIRONTREHPSTANTVDRTNHOLENLEAETAPLE 84
mORhuman 346 KRCFREFO...IPTSSSTIEQONSARIRONTREHPSTANTVDRTNHOLENLEAETAPLE 85
mORpig 347 KRCFREFO...IPTSSSTIEQONSARIRONTREHPSTANTVDRTNHOLENLEAETAPLE 86
mORws 340 KRCFREFO...IPTSSSTIEQONSARIRONTREHPSTANTVDRTNHOLENLEAETAPLE 87
ATla 310 KRCFREFO...IPTSSSTIEQONSARIRONTREHPSTANTVDRTNHOLENLEAETAPLE 81
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SEQ ID NO:

Figure 13